RAW SEQUENCE LISTING
ERROR REPORT

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Application Serial Number: 10/764,818

Source: 1FWO

Date Processed by STIC: 2/9/04

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http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

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1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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Revised 10/08/03

RAW SEQUENCE LISTING   DATE: 02/09/2004
PATENT APPLICATION: **US/10/764,818**   TIME: 10:36:04

        Input Set : **N:\FATIMA\10764818.txt**
        Output Set: **N:\CRF4\02062004\J764818.raw**

   3 <110> APPLICANT: ADViSYS
   5 <120> TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT
DECREASES CULLING IN
   6   HERD ANIMALS
   8 <130> FILE REFERENCE: 108328.00170 - AVSI-0033
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/764,818
C--> 10 <141> CURRENT FILING DATE: 2004-01-26
  10 <160> NUMBER OF SEQ ID NOS: 30
  12 <170> SOFTWARE: PatentIn version 3.1
  14 <210> SEQ ID NO: 1
  15 <211> LENGTH: 40
  16 <212> TYPE: PRT
  17 <213> ORGANISM: artificial sequence
  19 <220> FEATURE:
  20 <223> OTHER INFORMATION: This is the amino acid sequenc for HV-GHRH.
  22 <400> SEQUENCE: 1
  24 His Val Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Ala Gln
  25 1   5   10   15
  28 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Leu Asn Arg Gln Gln Gly
  29   20   25   30
  32 Glu Arg Asn Gln Glu Gln Gly Ala
  33   35   40
  36 <210> SEQ ID NO: 2
  37 <211> LENGTH: 40
  38 <212> TYPE: PRT
  39 <213> ORGANISM: artificial sequence
  41 <220> FEATURE:
  42 <223> OTHER INFORMATION: This is the amino acid sequenc for TI-GHRH.
  44 <400> SEQUENCE: 2
  46 Tyr Ile Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Ala Gln
  47 1   5   10   15
  50 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Leu Asn Arg Gln Gln Gly
  51   20   25   30
  54 Glu Arg Asn Gln Glu Gln Gly Ala
  55   35   40
  58 <210> SEQ ID NO: 3
  59 <211> LENGTH: 40
  60 <212> TYPE: PRT
  61 <213> ORGANISM: artificial sequence
  63 <220> FEATURE:
  64 <223> OTHER INFORMATION: This is the amino acid sequenc for TV-GHRH.
  66 <400> SEQUENCE: 3
  68 Tyr Val Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Ala Gln
  69 1   5   10   15

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Input Set : **N:\FATIMA\10764818.txt**
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72 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Leu Asn Arg Gln Gln Gly
73          20                  25                  30
76 Glu Arg Asn Gln Glu Gln Gly Ala
77          35                  40
80 <210> SEQ ID NO: 4
81 <211> LENGTH: 40
82 <212> TYPE: PRT
83 <213> ORGANISM: artificial sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: This is the amino acid sequenc for 15/27/28-GHRH.
88 <400> SEQUENCE: 4
90 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Ala Gln
91 1               5                  10                  15
94 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Leu Asn Arg Gln Gln Gly
95          20                  25                  30
98 Glu Arg Asn Gln Glu Gln Gly Ala
99          35                  40
102 <210> SEQ ID NO: 5
103 <211> LENGTH: 44
104 <212> TYPE: PRT
105 <213> ORGANISM: artificial sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: This is a consensus sequence for GHRH
110 <400> SEQUENCE: 5
112 Thr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
113 1               5                  10                  15
116 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly
117          20                  25                  30
120 Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu
121          35                  40
124 <210> SEQ ID NO: 6
125 <211> LENGTH: 40
126 <212> TYPE: PRT
127 <213> ORGANISM: artificial sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: This is the artificial sequence for GHRH (1-40)OH.
132 <220> FEATURE:
133 <221> NAME/KEY: MISC_FEATURE
134 <222> LOCATION: (1)..(1)
135 <223> OTHER INFORMATION: Xaa at position 1 may be tyrosine, or histidine
138 <220> FEATURE:
139 <221> NAME/KEY: MISC_FEATURE
140 <222> LOCATION: (2)..(2)
141 <223> OTHER INFORMATION: Xaa at position 2 may be alanine, valine, or isoleucine.
144 <220> FEATURE:
145 <221> NAME/KEY: MISC_FEATURE
146 <222> LOCATION: (15)..(15)
147 <223> OTHER INFORMATION: Xaa at position 15 may be alanine, valine, or isoleucine.
150 <220> FEATURE:
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151 <221> NAME/KEY: MISC_FEATURE
152 <222> LOCATION: (27)..(27)
153 <223> OTHER INFORMATION: Xaa at position 27 may be methionine, or leucine.
156 <220> FEATURE:
157 <221> NAME/KEY: MISC_FEATURE
158 <222> LOCATION: (28)..(28)
159 <223> OTHER INFORMATION: Xaa at position 28 may be serine or asparagine.
162 <220> FEATURE:
163 <221> NAME/KEY: MISC_FEATURE
164 <222> LOCATION: (34)..(34)
165 <223> OTHER INFORMATION: ARG may also be SER
168 <220> FEATURE:
169 <221> NAME/KEY: MISC_FEATURE
170 <222> LOCATION: (38)..(38)
171 <223> OTHER INFORMATION: Gln may also be Arg
174 <400> SEQUENCE: 6
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(handwritten annotation:) "Arg" can only represent itself, nothing else. Use "Xaa", instead, and explain in <2207–<2237 section

(handwritten annotations:) Same error use Xaa and explain

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W--> 176 Xaa Xaa Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Xaa Gln
177 1               5                   10                  15
180 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Xaa Xaa Arg Gln Gln Gly
181             20              25              30
184 Glu Arg Asn Gln Glu Gln Gly Ala
185     35              40
188 <210> SEQ ID NO: 7
189 <211> LENGTH: 323
190 <212> TYPE: DNA
191 <213> ORGANISM: artificial sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: This is a nucleic acid sequence of a eukaryotic promoter c5-
12.
196 <400> SEQUENCE: 7
197 cggccgtccg ccctcggcac catcctcacg acacccaaat atggcgacgg gtgaggaatg    60
199 gtggggagtt atttttagag cggtgaggaa ggtgggcagg cagcaggtgt tggcgctcta   120
201 aaaataactc ccgggagtta tttttagagc ggaggaatgg tggacaccca aatatggcga   180
203 cggttcctca cccgtcgcca tatttgggtg tccgccctcg gccggggccg cattcctggg   240
205 ggccgggcgg tgctcccgcc cgcctcgata aaaggctccg gggccggcgg cggcccacga   300
207 gctacccgga ggagcgggag gcg                                           323
210 <210> SEQ ID NO: 8
211 <211> LENGTH: 190
212 <212> TYPE: DNA
213 <213> ORGANISM: artificial sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Nucleic acid sequence of a hGH poly A tail.
218 <400> SEQUENCE: 8
219 gggtggcatc cctgtgaccc ctccccagtg cctctcctgg ccctggaagt tgccactcca    60
221 gtgcccacca gccttgtcct aataaaatta agttgcatca ttttgtctga ctaggtgtcc   120
223 ttctataata ttatggggtg gaggggggtg gtatggagca agggcaagt tgggaagaca    180
225 acctgtaggg                                                          190
228 <210> SEQ ID NO: 9
229 <211> LENGTH: 219
230 <212> TYPE: DNA
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 231 <213> ORGANISM: artificial sequence
 233 <220> FEATURE:
 234 <223> OTHER INFORMATION: This is the cDNA for Porcine GHRH.
 236 <400> SEQUENCE: 9
 237 atggtgctct gggtgttctt ctttgtgatc ctcaccctca gcaacagctc ccactgctcc      60
 239 ccacctcccc ctttgaccct caggatgcgg cggcacgtag atgccatctt caccaacagc     120
 241 taccggaagg tgctggccca gctgtccgcc cgcaagctgc tccaggacat cctgaacagg     180
 243 cagcagggag agaggaacca agagcaagga gcataatga                            219
 246 <210> SEQ ID NO: 10
 247 <211> LENGTH: 40
 248 <212> TYPE: PRT
 249 <213> ORGANISM: artificial sequence
 251 <220> FEATURE:
 252 <223> OTHER INFORMATION: This is the amino acid sequence for porcine GHRH.
 254 <400> SEQUENCE: 10
 256 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
 257 1               5                   10                  15
 260 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly
 261             20                  25                  30
 264 Glu Arg Asn Gln Glu Gln Gly Ala
 265         35                  40
 268 <210> SEQ ID NO: 11
 269 <211> LENGTH: 3534
 270 <212> TYPE: DNA
 271 <213> ORGANISM: artificial sequence
 273 <220> FEATURE:
 274 <223> OTHER INFORMATION: This is the nucleic acid sequence for the operatively linked
comp
 275        onents of the HV-GHRH plasmid.
 277 <400> SEQUENCE: 11
 278 gttgtaaaac gacggccagt gaattgtaat acgactcact atagggcgaa ttggagctcc      60
 280 accgcggtgg cggccgtccg ccctcggcac catcctcacg acacccaaat atggcgacgg     120
 282 gtgaggaatg gtggggagtt attttttagag cggtgaggaa ggtgggcagg cagcaggtgt     180
 284 tggcgctcta aaaataactc ccgggagtta tttttagagc ggaggaatgg tggacaccca     240
 286 aatatggcga cggttcctca cccgtcgcca tatttggggtg tccgccctcg gccgggggccg     300
 288 cattcctggg ggccgggcgg tgctcccgcc cgcctcgata aaaggctccg gggccggcgg     360
 290 cggcccacga gctacccgga ggagcgggag gcgccaagct ctagaactag tggatcccaa     420
 292 ggcccaactc cccgaaccac tcagggtcct gtggacagct cacctagctg ccatggtgct     480
 294 ctgggtgttc ttctttgtga tcctcaccct cagcaacagc tcccactgct ccccacctcc     540
 296 ccctttgacc ctcaggatgc ggcggcacgt agatgccatc ttcaccaaca gctaccggaa     600
 298 ggtgctggcc cagctgtccg cccgcaagct gctccaggac atcctgaaca ggcagcaggg     660
 300 agagaggaac caagagcaag gagcataatg actgcaggaa ttcgatatca agcttatcgg     720
 302 ggtggcatcc ctgtgacccc tccccagtgc ctctcctggc cctggaagtt gccactccag     780
 304 tgcccaccag ccttgtccta ataaaattaa gttgcatcat tttgtctgac taggtgtcct     840
 306 tctataatat tatgggggtgg aggggggtgg tatggagcaa ggggcaagtt gggaagacaa     900
 308 cctgtagggc ctgcggggtc tattgggaac caagctggag tgcagtggca caatcttggc     960
 310 tcactgcaat ctccgcctcc tgggttcaag cgattctcct gcctcagcct cccgagttgt    1020
 312 tgggattcca ggcatgcatg accaggctca gctaattttt gtttttttgg tagagacggg    1080
 314 gtttcaccat attggccagg ctggtctcca actcctaatc tcaggtgatc tacccacctt    1140
 316 ggcctcccaa attgctggga ttacaggcgt gaaccactgc tcccttccct gtccttctga    1200
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318 ttttaaaata actataccag caggaggacg tccagacaca gcataggcta cctggccatg   1260
320 cccaaccggt gggacatttg agttgcttgc ttggcactgt cctctcatgc gttgggtcca   1320
322 ctcagtagat gcctgttgaa ttcgataccg tcgacctcga gggggggccc ggtaccagct   1380
324 tttgttccct ttagtgaggg ttaatttcga gcttggcgta atcatggtca tagctgtttc   1440
326 ctgtgtgaaa ttgttatccg ctcacaattc cacacaacat acgagccgga agcataaagt   1500
328 gtaaagcctg gggtgcctaa tgagtgagct aactcacatt aattgcgttg cgctcactgc   1560
330 ccgctttcca gtcgggaaac ctgtcgtgcc agctgcatta atgaatcggc caacgcgcgg   1620
332 ggagaggcgg tttgcgtatt gggcgctctt ccgcttcctc gctcactgac tcgctgcgct   1680
334 cggtcgttcg ctgcggcga gcggtatcag ctcactcaaa ggcggtaata cggttatcca   1740
336 cagaatcagg ggataacgca ggaaagaaca tgtgagcaaa aggccagcaa aaggccagga   1800
338 accgtaaaaa ggccgcgttg ctggcgtttt tccataggct ccgcccccct gacgagcatc   1860
340 acaaaaatcg acgctcaagt cagaggtggc gaaacccgac aggactataa agataccagg   1920
342 cgtttccccc tggaagctcc ctcgtgcgct ctcctgttcc gaccctgccg cttaccggat   1980
344 acctgtccgc ctttctccct tcgggaagcg tggcgctttc tcatagctca cgctgtaggt   2040
346 atctcagttc ggtgtaggtc gttcgctcca agctgggctg tgtgcacgaa ccccccgttc   2100
348 agcccgaccg ctgcgcctta tccggtaact atcgtcttga gtccaacccg gtaagacacg   2160
350 acttatcgcc actggcagca gccactggta acaggattag cagagcgagg tatgtaggcg   2220
352 gtgctacaga gttcttgaag tggtggccta actacggcta cactagaaga acagtatttg   2280
354 gtatctgcgc tctgctgaag ccagttacct tcggaaaaag agttggtagc tcttgatccg   2340
356 gcaaacaaac caccgctggt agcggtggtt tttttgtttg caagcagcag attacgcgca   2400
358 gaaaaaaagg atctcaagaa gatcctttga tctttttctac ggggtctgac gctcagaaga   2460
360 actcgtcaag aaggcgatag aaggcgatgc gctgcgaatc gggagcggcg ataccgtaaa   2520
362 gcacgaggaa gcggtcagcc cattcgccgc caagctcttc agcaatatca cgggtagcca   2580
364 acgctatgtc ctgatagcgg tccgccacac ccagccggcc acagtcgatg aatccagaaa   2640
366 agcggccatt ttccaccatg atattcggca agcaggcatc gccatgggtc acgacgagat   2700
368 cctcgccgtc gggcatgcgc gccttgagcc tggcgaacag ttcggctggc gcgagcccct   2760
370 gatgctcttc gtccagatca tcctgatcga caagaccggc ttccatccga gtacgtgctc   2820
372 gctcgatgcg atgtttcgct tggtggtcga atgggcaggt agccggatca agcgtatgca   2880
374 gccgccgcat tgcatcagcc atgatggata ctttctcggc aggagcaagg tgagatgaca   2940
376 ggagatcctg ccccggcact tcgcccaata gcagccagtc ccttcccgct tcagtgacaa   3000
378 cgtcgagcac agctgcgcaa ggaacgcccg tcgtggccag ccacgatagc cgcgctgcct   3060
380 cgtcctgcag ttcattcagg gcaccggaca ggtcggtctt gacaaaaaga accgggcgcc   3120
382 cctgcgctga cagccggaac acggcggcat cagagcagcc gattgtctgt tgtgcccagt   3180
384 catagccgaa tagcctctcc acccaagcgg ccggagaacc tgcgtgcaat ccatcttgtt   3240
386 caatcatgcg aaacgatcct catcctgtct cttgatcaga tcttgatccc ctgcgccatc   3300
388 agatccttgg cggcaagaaa gccatccagt ttactttgca gggcttccca accttaccag   3360
390 agggcgcccc agctggcaat tccggttcgc ttgctgtcca taaaaccgcc cagtctagca   3420
392 actgttggga agggcgatcg gtgcgggcct cttcgctatt acgccagctg gcgaaagggg   3480
394 gatgtgctgc aaggcgatta agttgggtaa cgccagggtt ttcccagtca cgac          3534
397 <210> SEQ ID NO: 12
398 <211> LENGTH: 3534
399 <212> TYPE: DNA
400 <213> ORGANISM: artificial sequence
402 <220> FEATURE:
403 <223> OTHER INFORMATION: Nucleic acid sequence for the TI-GHRH plasmid.
405 <400> SEQUENCE: 12
406 gttgtaaaac gacggccagt gaattgtaat acgactcact atagggcgaa ttggagctcc      60
408 accgcggtgg cggccgtccg ccctcggcac catcctcacg acacccaaat atggcgacgg     120
410 gtgaggaatg gtggggagtt atttttagag cggtgaggaa ggtgggcagg cagcaggtgt     180
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/09/2004
PATENT APPLICATION: US/10/764,818   TIME: 10:36:05

Input Set : **N:\FATIMA\10764818.txt**
Output Set: **N:\CRF4\02062004\J764818.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 1,2,15,27,28

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY   DATE: 02/09/2004
PATENT APPLICATION: **US/10/764,818**   TIME: 10:36:05

Input Set : **N:\FATIMA\10764818.txt**
Output Set: **N:\CRF4\02062004\J764818.raw**

```
L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
M:341 Repeated in SeqNo=6
```